

 [ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Proteomics tools](#)[Swiss-Prot](#)Search for Please help us to better understand your needs and expectations regarding ExPASy and complete our [online survey](#)!

Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq3, (205 residues)

Sequence 2: UserSeq1, (205 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

100.0% identity in 205 residues overlap; Score: 1078.0; Gap frequency: 0.0%

UserSeq3,	1	MTENILRKSDEEIQKEITARVKALESMLEQGILTTSMDRMAEIIYENEVGPLGAKVVV
UserSeq1,	1	MTENILRKSDEEIQKEITARVKALESMLEQGILTTSMDRMAEIIYENEVGPLGAKVVV

UserSeq3,	61	KAWTDPEFFKKRLLADGTEACKELGIGGLQGEDMMWVENTDEVHHVVVCTLCSCYPWPVLG
UserSeq1,	61	KAWTDPEFFKKRLLADGTEACKELGIGGLQGEDMMWVENTDEVHHVVVCTLCSCYPWPVLG

UserSeq3,	121	LPPNWFKEPQYRSRVVREPRQLLKEEFGFEVPPSKEIKVWDSSEMRFVVLQRPAGTDG
UserSeq1,	121	LPPNWFKEPQYRSRVVREPRQLLKEEFGFEVPPSKEIKVWDSSEMRFVVLQRPAGTDG

UserSeq3,	181	WSEEELATLVTRESMIGVEPAKAVA
UserSeq1,	181	WSEEELATLVTRESMIGVEPAKAVA

22.2% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0.0%

UserSeq3, 65 DPEFKKRLLDGTEACKE
UserSeq1, 128 EPQYRSRVVREPRQLLKE
 * * **

22.2% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0.0%

UserSeq3, 128 EPQYRSRVVREPRQLLKE
UserSeq1, 65 DPEFKKRLLDGTEACKE
 * * **

20.0% identity in 20 residues overlap; Score: 23.0; Gap frequency: 0.0%

UserSeq3, 44 EIIYENEVGPHLGAKVVVKAW
UserSeq1, 141 QLLKEEFGFEVPPSKEIKVW
 * * * *

20.0% identity in 20 residues overlap; Score: 23.0; Gap frequency: 0.0%

UserSeq3, 141 QLLKEEFGFEVPPSKEIKVW
UserSeq1, 44 EIIYENEVGPHLGAKVVVKAW
 * * * *

36.4% identity in 11 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq3, 64 TDPEFKKRLLA
UserSeq1, 9 SDEEIQKEITA
 * * * *

36.4% identity in 11 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq3, 9 SDEEIQKEITA
UserSeq1, 64 TDPEFKKRLLA
 * * * *

40.0% identity in 10 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq3, 182 SEEELATLVT
UserSeq1, 9 SDEEIQKEIT
 * ** *

40.0% identity in 10 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq3, 9 SDEEIQKEIT
UserSeq1, 182 SEEELATLVT

* ** *

31.2% identity in 16 residues overlap; Score: 20.0; Gap frequency: 0.0%

UserSeq3, 142 LLKEEFGFEVPPSKEI
UserSeq1, 189 LVTRESMIGVEPAKAV
* * * * *

31.2% identity in 16 residues overlap; Score: 20.0; Gap frequency: 0.0%

UserSeq3, 189 LVTRESMIGVEPAKAV
UserSeq1, 142 LLKEEFGFEVPPSKEI
* * * * *

19.0% identity in 21 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 1 MTENILRKSDEEIQKEITARV
UserSeq1, 38 MIDRMAEIIYENEVGPHLGAKV
* * * *

40.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 181 WSEEE
UserSeq1, 63 WTDPE
* *

35.3% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 143 LKEEFGFEVPPSKEIKV
UserSeq1, 42 MAEIIYENEVGPHLGAKV
* ** * **

40.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 63 WTDPE
UserSeq1, 181 WSEEE
* *

17.6% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 1 MTENILRKSDEEIQKEI
UserSeq1, 34 LTTSMIDRMAEIIYENEV
* * *

17.6% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      34 LTTSMIDRMAEIIYENEV
UserSeq1,       1 MTENILRKSDDEEIQKEI
                *      *      *
```

19.0% identity in 21 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      38 MIDRMAEIIYENEVGPHLGAKV
UserSeq1,       1 MTENILRKSDDEEIQKEITARV
                *      *      *  *
```

35.7% identity in 14 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,     183 EEELATLVTRESMI
UserSeq1,     15 KEITARVKALESML
                *  *      ***
```

35.7% identity in 14 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      15 KEITARVKALESML
UserSeq1,    183 EEELATLVTRESMI
                *  *      ***
```

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Proteomics tools](#)[Swiss-Prot](#)